

SEQUENCE LISTING

<110> BOYLE, WILLIAM

<120> OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS

<130> A-451K REV 09-10-03 54SEQ

<140> US 09/721,212

<141> 2000-11-21

<150> US 09/052,521

<151> 1998-03-30

<150> US 08/880,855

<151> 1997-06-23

<150> US 08/842,842

<151> 1997-04-16

<160> 54

<170> PatentIn version 3.1

<210> 1

<211> 2295

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (158) .. (1105)

<223>

<400> 1

gagctcggat ccactactcg acccacgcgt ccggccagga cctctgtgaa ccggtcgggg	60
cgggggccgc ctggccggga gtctgctcgg cgggtgggtgg ccgaggaagg gagagaacga	120
tcgcggagca gggcgcccga actccgggcg ccgcgcc atg cgc cgg gcc agc cga	175
Met Arg Arg Ala Ser Arg	
1 5	
gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc	223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro	
10 15 20	
ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct	271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala	
25 30 35	
ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg	319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu	
40 45 50	
ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac	367
Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr	
55 60 65 70	
ttt cga gcg cag atg gat cct aac aga ata tca gaa gac agc act cac	415
Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His	
75 80 85	
tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt ttg cag gac	463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp	
90 95 100	
tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc agg agg atg	511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met	
105 110 115	
aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa cac att gtg	559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val	
120 125 130	
ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa ggc tca tgg	607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp	
135 140 145 150	
ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca ttt gca cac	655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His	
155 160 165	
ctc acc atc aat gct gcc agc atc cca tcg ggt tcc cat aaa gtc act	703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr	
170 175 180	
ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc tct aac atg	751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met	
185 190 195	
acg tta agc aac gga aaa cta agg gtt aac caa gat ggc ttc tat tac	799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr	
200 205 210	

ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tcg gga agc gta Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val 215 220 225 230	847
cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa acc agc atc Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile 235 240 245	895
aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc acg aaa aac Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn 250 255 260	943
tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat gtt ggg gga Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly 265 270 275	991
ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag gtg tcc aac Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn 280 285 290	1039
cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt ggg gct ttc Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 295 300 305 310	1087
aaa gtt cag gac ata gac tgagactcat ttcgtggaac attagcatgg Lys Val Gln Asp Ile Asp 315	1135
atgtcctaga tgttttgaaa cttcttaaaa aatggatgat gtctatacat gtgtaagact	1195
actaagagac atggcccacg gtgtatgaaa ctcacagccc tctctcttga gcctgtacag	1255
gttgtgtata tgtaaagtcc ataggtgatg ttagattcat ggtgattaca caacggtttt	1315
acaattttgt aatgatttcc tagaattgaa ccagattggg agaggtattc cgatgcttat	1375
gaaaaactta cacgtgagct atggaagggg gtcacagtct ctgggtctaa cccctggaca	1435
tgtgccactg agaaccttga aattaagagg atgccatgtc attgcaaaga aatgatagtg	1495
tgaaggggta agttcttttg aattgttaca ttgcgctggg acctgcaa atagttctttt	1555
tttctaata gaagagaaaa atatatgtat ttttatataa tgtctaaagt tatatttcag	1615
gtgtaatgtt ttctgtgcaa agttttgtaa attatatattg tgctatagta tttgattcaa	1675
aatattttaa aatgtctcac tgttgacata tttaattgtt taaatgtaca gatgtattta	1735
actggtgcac tttgtaattc ccctgaaggt actcgtagct aagggggcag aatactgttt	1795
ctggtgacca catgtagttt atttctttat tcttttttaac ttaatagagt cttcagactt	1855
gtcaaaacta tgcaagcaaa ataaataaat aaaaataaaa tgaatacctt gaataataag	1915
taggatgttg gtcaccaggt gcctttcaaa tttagaagct aattgacttt aggagctgac	1975
atagccaaaa aggatacata ataggctact gaaatctgtc aggagtattt atgcaattat	2035
tgaacaggtg tcttttttta caagagctac aaattgtaaa ttttgtttct tttttttccc	2095
atagaaaatg tactatagtt tatcagccaa aaaacaatcc actttttaat ttagtgaaag	2155
ttattttatt atactgtaca ataaaagcat tgtctctgaa tgtaatttt ttggtacaaa	2215

aaataaatTTT gtacgaaaac ctgaaaaaaaa aaaaaaaaaa aaaaaaaagg gcggccgctc 2275
tagagggccc tattctatag 2295

<210> 2

<211> 316

<212> PRT

<213> Mus musculus

<400> 2

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu
1				5					10					15	
Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro
			20					25					30		
Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser
		35					40					45			
Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser
	50					55					60				
Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile
65					70					75					80
Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu
				85					90					95	
Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro
			100					105					110		
Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys
		115					120					125			
Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala
	130					135					140				
Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu
145					150					155					160
Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser
				165					170					175	
Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp
			180					185					190		

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
305 310 315

<210> 3

<211> 2271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (185)..(1135)

<223>

<400> 3

aagcttggtgta ccgagctcgg atccactact cgacccacgc gtccgcgcgc cccaggagcc	60
aaagccggggc tccaagtcgg cgccccacgt cgagggtccg ccgcagcctc cggagttggc	120
cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag	180
cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg	229
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser	
1 5 10 15	

gag	gag	atg	ggc	ggc	ggc	ccc	gga	gcc	ccg	cac	gag	ggc	ccc	ctg	cac	277
Glu	Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	
			20						25					30		
gcc	ccg	ccg	ccg	cct	gcg	ccg	cac	cag	ccc	ccc	gcc	gcc	tcc	cgc	tcc	325
Ala	Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	
			35					40					45			
atg	ttc	gtg	gcc	ctc	ctg	ggg	ctg	ggg	ctg	ggc	cag	ggt	gtc	tgc	agc	373
Met	Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	
		50				55						60				
gtc	gcc	ctg	ttc	ttc	tat	ttc	aga	gcg	cag	atg	gat	cct	aat	aga	ata	421
Val	Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	
	65				70						75					
tca	gaa	gat	ggc	act	cac	tgc	att	tat	aga	att	ttg	aga	ctc	cat	gaa	469
Ser	Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	
80				85						90					95	
aat	gca	gat	ttt	caa	gac	aca	act	ctg	gag	agt	caa	gat	aca	aaa	tta	517
Asn	Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	
				100					105					110		
ata	cct	gat	tca	tgt	agg	aga	att	aaa	cag	gcc	ttt	caa	gga	gct	gtg	565
Ile	Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	
			115					120					125			
caa	aag	gaa	tta	caa	cat	atc	gtt	gga	tca	cag	cac	atc	aga	gca	gag	613
Gln	Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	
		130					135					140				
aaa	gcg	atg	gtg	gat	ggc	tca	tgg	tta	gat	ctg	gcc	aag	agg	agc	aag	661
Lys	Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	
	145					150					155					
ctt	gaa	gct	cag	cct	ttt	gct	cat	ctc	act	att	aat	gcc	acc	gac	atc	709
Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	
160				165						170					175	
cca	tct	ggt	tcc	cat	aaa	gtg	agt	ctg	tcc	tct	tgg	tac	cat	gat	cgg	757
Pro	Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	
				180					185					190		
ggt	tgg	gcc	aag	atc	tcc	aac	atg	act	ttt	agc	aat	gga	aaa	cta	ata	805
Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	
			195					200					205			
gtt	aat	cag	gat	ggc	ttt	tat	tac	ctg	tat	gcc	aac	att	tgc	ttt	cga	853
Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	
		210				215						220				
cat	cat	gaa	act	tca	gga	gac	cta	gct	aca	gag	tat	ctt	caa	cta	atg	901
His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	
	225					230					235					
gtg	tac	gtc	act	aaa	acc	agc	atc	aaa	atc	cca	agt	tct	cat	acc	ctg	949
Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	
240					245					250					255	
atg	aaa	gga	gga	agc	acc	aag	tat	tgg	tca	ggg	aat	tct	gaa	ttc	cat	997
Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	
				260					265					270		

ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag 1045
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
275 280 285

gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
290 295 300

gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat 1135
Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

tgagccccag tttttggagt gttatgtatt tcctggatgt ttggaaacat tttttaaaac 1195

aagccaagaa agatgtatat aggtgtgtga gactactaag aggcattggcc ccaacggtac 1255

acgactcagt atccatgctc ttgaccttgt agagaacacg cgtattttaca gccagtggga 1315

gatgttagac tcatggtgtg ttacacaatg gtttttaaat tttgtaatga attcctagaa 1375

ttaaaccaga ttggagcaat tacggggtga ccttatgaga aactgcatgt gggctatggg 1435

agggggttggc ccctgggtcat gtgccccttc gcagctgaag tggagagggg gtcattctagc 1495

gcaattgaag gatcatctga aggggcaaat tcttttgaat tgttacatca tgctggaacc 1555

tgcaaaaaat acttttttcta atgaggagag aaaatatatg tattttttata taatatctaa 1615

agttatatatt cagatgtaat gttttctttg caaagtattg taaattatat ttgtgctata 1675

gtatttgatt caaaatattt aaaaatgtct tgctgttgac atattttaatg ttttaaatgt 1735

acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag 1795

gggaaaaaaa tggtgtttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt 1855

aatagattttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata 1915

ataagcagga tggtggccac caggtgcctt tcaaatttag aaactaattg actttagaaa 1975

gctgacattg ccaaaaagga tacataatgg gccactgaaa tctgtcaaga gtagttatat 2035

aattggtgaa caggtgtttt tccacaagtg ccgcaaattg tacctttttt ttttttcaa 2095

aatagaaaaag ttatttagtgg tttatcagca aaaaagtcca attttaattt agtaaattgt 2155

atcttatact gtacaataaa aacattgcct ttgaatgtta attttttggt acaaaaaataa 2215

atttatatga aaaaaaaaaa aaaagggcgg ccgctctaga gggccctatt ctatag 2271

<210> 4

<211> 317

<212> PRT

<213> Homo sapiens

<400> 4

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu
1				5					10					15	
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala
		20						25					30		
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met
		35					40					45			
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val
	50					55					60				
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser
65					70					75					80
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn
				85					90					95	
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile
			100					105					110		
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln
		115					120					125			
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys
	130					135					140				
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu
145					150					155					160
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro
				165					170					175	
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly
			180					185					190		
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val
		195					200					205			
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His
	210					215					220				
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val
225					230					235					240
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met
				245					250					255	

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

<210> 5

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 5
gttctcctca tatggatcca aaccgtatatt ctgaagacag cactcactgc tt 52

<210> 6

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 6
tacgcactcc gcggttagtc tatgtcctga actttga 37

<210> 7

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 7
atttgattct agaaggagga ataacatatg catgaaaacg caggtctgca g 51

<210> 8

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 8
tatccgcgga tcctcgagtt agtctatgtc ctgaactttg aa 42

<210> 9

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 9
atttgattct agaaggagga ataacatatg tctgaagaca ctctgccgga ctcc 54

<210> 10

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 10
tatccgcgga tcctcgagtt agtctatgtc ctgaactttg aa 42

<210> 11

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 11

atttgattct agaaggagga ataacatatg aaacaagctt ttcagggg

48

<210> 12

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 12

tatccgcgga tcctcgagtt agtctatgtc ctgaactttg aa

42

<210> 13

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 13

atttgattct agaaggagga ataacatatg aaagaactgc agcacattgt g

51

<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 14
tatccgcgga tcctcgagtt agtctatgtc ctgaactttg aa 42

<210> 15

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 15
atttgattct agaaggagga ataacatatg cagcgtttct ctggtgctcc a 51

<210> 16

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 16
tatccgcgga tcctcgagtt agtctatgtc ctgaactttg aa 42

<210> 17

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 17
gttctcctca tatggaaggt tcttggttgg atgtggccca 40

<210> 18

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 18
tacgcactcc gcggttagtc tatgtcctga actttga 37

<210> 19

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 19
gttctcctca tatgcgtggt aaacctgaag ctcaaccatt tgca 44

<210> 20

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 20
tacgcactcc gcggttagtc tatgtcctga actttga 37

<210> 21

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 21
gttctcctca tatgaaacct gaagctcaac catttgcaca cctcaccatc aat 53

<210> 22

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 22

tacgcactcc gcggttagtc tatgtcctga actttga

37

<210> 23

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 23

gttctcctca tatgcattta actattaacg ctgcatctat cccatcgggt tcccataaag

60

tcact

65

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 24

tacgcactcc gcggttagtc tatgtcctga actttga

37

<210> 25

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 25

gttctcctca tatgactatt aacgctgcat ctatcccatc gggttcccat aaagtcact 59

<210> 26

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 26

tacgcactcc gcggttagtc tatgtcctga actttga 37

<210> 27

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 27

cctctaggcc tgtactttcg agcgagatg 30

<210> 28

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 28

cctctgcggc cgcgtctatg tcctgaactt tg 32

<210> 29

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 29

cctctctcga gtggacaacc cagaagcctg aggcccagcc atttgc

46

<210> 30

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 30

cctctgcggc cgcgtctatg tcctgaactt tg

32

<210> 31

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 31

agcttccacc atgaacaagt ggctgtgctg cgcactcctg gtgctcctgg acatca

56

<210> 32

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 32

tcgatgatgt ccaggagcac caggagtgcg cagcacagcc acttggtcat ggtgga 56

<210> 33

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 33

Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser
1 5 10 15

Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser
20 25

<210> 34

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 34

Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser
1 5 10 15

Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Cys
20 25

<210> 35

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 35

Val	Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu
1				5					10					15	

Met

<210> 36

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 36

Val	Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu
1				5					10					15	

Met Cys

<210> 37

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 37

tctccaagct tgtgactctc caggctcactc c

31

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 38

tctccgcggc cgcgtaagcc tgggcctcat tgggtg 36

<210> 39

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 39

ctagcaccat gaacaagtgg ctgtgctgcg cactcctggt gtcctggac atcattgaat 60

ggacaaccca ga 72

<210> 40

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 40

agcttctggg ttgtccattc aatgatgtcc aggagcacca ggagtgcgca gcacagccac 60

ttgttcatgg tg 72

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 41

Met Asp Pro Asn Arg Gln Asp Ile Asp
1 5

<210> 42

<211> 2071

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<220>

<221> CDS

<222> (36)..(1910)

<223>

<400> 42

actcgaccca	cgcggtccgcc	cgcccgcacc	gcgcc	atg	gac	ccg	cg	gcc	cgg		53					
				Met	Asp	Pro	Arg	Ala	Arg							
				1				5								
cg	cg	cg	cag	ctg	ccc	gcg	ccg	ctg	ctg	gcg	ctc	tgc	gtg	ctg	ctc	101
Arg	Arg	Arg	Gln	Leu	Pro	Ala	Pro	Leu	Leu	Ala	Leu	Cys	Val	Leu	Leu	
			10					15					20			
gtt	cca	ctg	cag	gtg	act	ctc	cag	gtc	act	cct	cca	tgc	acc	cag	gag	149
Val	Pro	Leu	Gln	Val	Thr	Leu	Gln	Val	Thr	Pro	Pro	Cys	Thr	Gln	Glu	
		25					30					35				
agg	cat	tat	gag	cat	ctc	gga	cg	tgt	tgc	agc	aga	tgc	gaa	cca	gga	197
Arg	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	Ser	Arg	Cys	Glu	Pro	Gly	
	40					45					50					
aag	tac	ctg	tcc	tct	aag	tgc	act	cct	acc	tcc	gac	agt	gtg	tgt	ctg	245
Lys	Tyr	Leu	Ser	Ser	Lys	Cys	Thr	Pro	Thr	Ser	Asp	Ser	Val	Cys	Leu	
55					60					65				70		
ccc	tgt	ggc	ccc	gat	gag	tac	ttg	gac	acc	tgg	aat	gaa	gaa	gat	aaa	293
Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Thr	Trp	Asn	Glu	Glu	Asp	Lys	
				75					80					85		
tgc	ttg	ctg	cat	aaa	gtc	tgt	gat	gca	ggc	aag	gcc	ctg	gtg	gcg	gtg	341
Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Ala	Gly	Lys	Ala	Leu	Val	Ala	Val	
			90					95					100			
gat	cct	ggc	aac	cac	acg	gcc	ccg	cgt	cg	tgt	gct	tgc	acg	gct	ggc	389

Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg	Cys	Ala	Cys	Thr	Ala	Gly	
		105					110					115				
tac	cac	tgg	aac	tca	gac	tgc	gag	tgc	tgc	cgc	agg	aac	acg	gag	tgt	437
Tyr	His	Trp	Asn	Ser	Asp	Cys	Glu	Cys	Cys	Arg	Arg	Asn	Thr	Glu	Cys	
		120				125					130					
gca	cct	ggc	ttc	gga	gct	cag	cat	ccc	ttg	cag	ctc	aac	aag	gat	acg	485
Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu	Gln	Leu	Asn	Lys	Asp	Thr	
135					140					145					150	
gtg	tgc	aca	ccc	tgc	ctc	ctg	ggc	ttc	ttc	tca	gat	gtc	ttt	tcg	tcc	533
Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe	Ser	Asp	Val	Phe	Ser	Ser	
				155					160					165		
aca	gac	aaa	tgc	aaa	cct	tgg	acc	aac	tgc	acc	ctc	ctt	gga	aag	cta	581
Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Leu	Gly	Lys	Leu	
			170					175					180			
gaa	gca	cac	cag	ggg	aca	acg	gaa	tca	gat	gtg	gtc	tgc	agc	tct	tcc	629
Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp	Val	Val	Cys	Ser	Ser	Ser	
		185					190					195				
atg	aca	ctg	agg	aga	cca	ccc	aag	gag	gcc	cag	gct	tac	ctg	ccc	agt	677
Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	Gln	Ala	Tyr	Leu	Pro	Ser	
	200					205					210					
ctc	atc	gtt	ctg	ctc	ctc	ttc	atc	tct	gtg	gta	gta	gtg	gct	gcc	atc	725
Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	Val	Val	Val	Ala	Ala	Ile	
215					220					225					230	
atc	ttc	ggc	gtt	tac	tac	agg	aag	gga	ggg	aaa	gcg	ctg	aca	gct	aat	773
Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	Lys	Ala	Leu	Thr	Ala	Asn	
				235					240					245		
ttg	tgg	aat	tgg	gtc	aat	gat	gct	tgc	agt	agt	cta	agt	gga	aat	aag	821
Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	Ser	Leu	Ser	Gly	Asn	Lys	
			250					255					260			
gag	tcc	tca	ggg	gac	cgt	tgt	gct	ggc	tcc	cac	tcg	gca	acc	tcc	agt	869
Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	His	Ser	Ala	Thr	Ser	Ser	
		265					270					275				
cag	caa	gaa	gtg	tgt	gaa	ggc	atc	tta	cta	atg	act	cgg	gag	gag	aag	917
Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	Met	Thr	Arg	Glu	Glu	Lys	
	280					285					290					
atg	gtt	cca	gaa	gac	ggc	gct	gga	gtc	tgt	ggg	cct	gtg	tgt	gcg	gca	965
Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	Gly	Pro	Val	Cys	Ala	Ala	
295					300					305					310	
ggc	ggg	ccc	tgg	gca	gaa	gtc	aga	gat	tct	agg	acg	ttc	aca	ctg	gtc	1013
Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	Arg	Thr	Phe	Thr	Leu	Val	
				315					320					325		
agc	gag	gtt	gag	acg	caa	gga	gac	ctc	tcg	agg	aag	att	ccc	aca	gag	1061
Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	Arg	Lys	Ile	Pro	Thr	Glu	
			330					335					340			
gat	gag	tac	acg	gac	cgg	ccc	tcg	cag	cct	tcg	act	ggc	tca	ctg	ctc	1109
Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Ser	Gln	Pro	Ser	Thr	Gly	Ser	Leu	Leu	
		345					350					355				
cta	atc	cag	cag	gga	agc	aaa	tct	ata	ccc	cca	ttc	cag	gag	ccc	ctg	1157

Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	Pro	Phe	Gln	Glu	Pro	Leu	
360						365					370					
gaa	gtg	ggg	gag	aac	gac	agt	tta	agc	cag	tgt	ttc	acc	ggg	act	gaa	1205
Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Glu	
375					380					385					390	
agc	acg	gtg	gat	tct	gag	ggc	tgt	gac	ttc	act	gag	cct	ccg	agc	aga	1253
Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	Thr	Glu	Pro	Pro	Ser	Arg	
				395					400					405		
act	gac	tct	atg	ccc	gtg	tcc	cct	gaa	aag	cac	ctg	aca	aaa	gaa	ata	1301
Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	His	Leu	Thr	Lys	Glu	Ile	
			410					415					420			
gaa	ggt	gac	agt	tgc	ctc	ccc	tgg	gtg	gtc	agc	tcc	aac	tca	aca	gat	1349
Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	Ser	Ser	Asn	Ser	Thr	Asp	
		425					430					435				
ggc	tac	aca	ggc	agt	ggg	aac	act	cct	ggg	gag	gac	cat	gaa	ccc	ttt	1397
Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	Glu	Asp	His	Glu	Pro	Phe	
	440					445					450					
cca	ggg	tcc	ctg	aaa	tgt	gga	cca	ttg	ccc	cag	tgt	gcc	tac	agc	atg	1445
Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Ser	Met	
455					460					465					470	
ggc	ttt	ccc	agt	gaa	gca	gca	gcc	agc	atg	gca	gag	gcg	gga	gta	cgg	1493
Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	Ala	Glu	Ala	Gly	Val	Arg	
				475					480					485		
ccc	cag	gac	agg	gct	gat	gag	agg	gga	gcc	tca	ggg	tcc	ggg	agc	tcc	1541
Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	Ser	Gly	Ser	Gly	Ser	Ser	
			490					495					500			
ccc	agt	gac	cag	cca	cct	gcc	tct	ggg	aac	gtg	act	gga	aac	agt	aac	1589
Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn	
		505					510					515				
tcc	acg	ttc	atc	tct	agc	ggg	cag	gtg	atg	aac	ttc	aag	ggg	gac	atc	1637
Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile	
	520					525					530					
atc	gtg	gtg	tat	gtc	agc	cag	acc	tcg	cag	gag	ggc	ccg	ggg	tcc	gca	1685
Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Pro	Gly	Ser	Ala	
535					540					545					550	
gag	ccc	gag	tcg	gag	ccc	gtg	ggc	cgc	cct	gtg	cag	gag	gag	acg	ctg	1733
Glu	Pro	Glu	Ser	Glu	Pro	Val	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	
				555					560					565		
gca	cac	aga	gac	tcc	ttt	gcg	ggc	acc	gcg	ccg	gcg	ttc	ccc	gac	gtc	1781
Ala	His	Arg	Asp	Ser	Phe	Ala	Gly	Thr	Ala	Pro	Arg	Phe	Pro	Asp	Val	
			570					575					580			
tgt	gcc	acc	ggg	gct	ggg	ctg	cag	gag	cag	ggg	gca	ccc	cgg	cag	aag	1829
Cys	Ala	Thr	Gly	Ala	Gly	Leu	Gln	Glu	Gln	Gly	Ala	Pro	Arg	Gln	Lys	
		585				590						595				
gac	ggg	aca	tcg	cgg	ccg	gtg	cag	gag	cag	ggg	ggg	gcg	cag	act	tca	1877
Asp	Gly	Thr	Ser	Arg	Pro	Val	Gln	Glu	Gln	Gly	Gly	Ala	Gln	Thr	Ser	
	600					605					610					
ctc	cat	acc	cag	ggg	tcc	gga	caa	tgt	gca	gaa	tgac	ctcacc	ttctctgtct			1930

Leu His Thr Gln Gly Ser Gly Gln Cys Ala Glu
615 620 625
gccctgggtg cagggcacca gtgcctttcc aaaaacatgg tgtagctagc cactgtgcac 1990
ctcctcactg gtgcaggctg ctggcatggg gatggagccc acctctcact tcctccagtg 2050
cccctctcct ctgcctccta c 2071

<210> 43

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 43

Met Asp Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
1 5 10 15

Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr
20 25 30

Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
35 40 45

Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
50 55 60

Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
65 70 75 80

Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
85 90 95

Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
100 105 110

Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
115 120 125

Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
130 135 140

Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
145 150 155 160

Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
165 170 175

Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
180 185 190

Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
195 200 205

Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
210 215 220

Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
225 230 235 240

Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
245 250 255

Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
260 265 270

His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
275 280 285

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
290 295 300

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
305 310 315 320

Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
340 345 350

Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
355 360 365

Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln
370 375 380

Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe
385 390 395 400

Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys
405 410 415

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
420 425 430

Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
450 455 460

Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
465 470 475 480

Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
500 505 510

Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
530 535 540

Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln
580 585 590

Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln
595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
610 615 620

Glu
625

<210> 44

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 44

Met	His	Glu	Asn	Ala	Gly	Gln	Asp	Ile	Asp
1				5					10

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 45

Met	Ser	Glu	Asp	Thr	Leu	Gln	Asp	Ile	Asp
1				5					10

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 46

Met	Lys	Gln	Ala	Phe	Gln	Gln	Asp	Ile	Asp
1				5					10

<210> 47

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 47

Met Lys Glu Leu Gln His Gln Asp Ile Asp
1 5 10

<210> 48

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 48

Met Gln Arg Phe Ser Gly Gln Asp Ile Asp
1 5 10

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 49

Met Glu Gly Ser Trp Gln Asp Ile Asp
1 5

<210> 50

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 50

Met Arg Gly Lys Pro Gln Asp Ile Asp
1 5

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 51

Met Lys Pro Glu Ala Gln Asp Ile Asp
1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 52

Met His Leu Thr Ile Gln Asp Ile Asp
1 5

<210> 53

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 53

Met Thr Ile Asn Ala Gln Asp Ile Asp
1 5

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 54

Lys Leu Val Thr Leu Gln Val Thr Pro
1 5